



02/18/97

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Rodriguez, Moses
Miller, David J.
Asakura, Kunihiro

(ii) TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM REMYELINATION
USING MONOCLONAL AUTOANTIBODIES

(iii) NUMBER OF SEQUENCES: 37

(iv) CORRESPONDENCE ADDRESS:

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Floor
(C) CITY: Hackensack
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(E) COUNTRY: USA
(F) ZIP: 07601

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/692,084
(B) FILING DATE: 08-AUG-1996
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/236,520
(B) FILING DATE: 29-APR-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Jackson Esq., David A.
(B) REGISTRATION NUMBER: 26,742
(C) REFERENCE/DOCKET NUMBER: 1199-1-001 CIP

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201-487-5800
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGGATGGA GATGGATCTT TCTTTTCCTC CTGTCAGGAA CTGCAGGTGT CCATTGCCAG	60
GTTTCAGCTGC AGCAGTCTGG ACCTGAGCTG GTGAAGCCTG GGGCTTTAGT GAAGATATCC	120
TGCAAGGCTT CTGGTTACAC CTTTACAAGC TACGATATAA ACTGGGTGAA GCAGAGGCCT	180
GGACAGGGAC TTGAGTGGAT TGGATGGATT TATCCTGGAG ATGGTAGTAC TAAGTACAAT	240
GAGAAATTCA AGGGCAAGGC CACACTGACT GCAGACAAAT CCTCCAGCAC AGCCTACATG	300
CAGCTCAGCA GCCTGACTTC TGAGAACTCT GCAGTCTATT TCTGTGCAAG AGGGGCCAGG	360
TTCTACTGGT ACTTCGATGT CTGGGGCGCA GGGACCACGG TCACCGTCTC CTCAGAGAGT	420

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGCTGTCT TGGGGCTGCT CTTCTGCCTG GTGACATTCC CAAGCTGTGT CCTATCCCAG	60
GTGCAGCTGA AGCAGTCAGG ACCTGGCCTA GTGCAGCCCT CACAGAGCCT GTCCATCACC	120
TGCACAGTCT CTGGTTTCTC ATTAAGTAGC TATGGTGTAC ACTGGGTTCG CCAGTCTCCA	180

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GGAAAGGGTC TGGAGTGGCT GGGAGTGATA TGGAGTGGTG GAAGCACAGA CTATAATGCA	240
GCTTTCATAT CCAGACTGAG CATCAGCAAG GACGCTTCCA AGAGCCAAGT TTTCTTTTAAA	300
ATGAACAGTC TGCACGCTAC TGACACAGCC ATATATTATT GTGCCAGAGA CTACGGTAGT	360
AGGGGGGACT ACTGGGGTCA AGGAACCTCA GTCACCGTCT CCTCA	405

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGAAGTTGT GGTAAACTG GGTTTTTCTT TTAACACTTT TACATGGTAT CCAGTGTGAG	60
GTGAAGCTGG TGGAATCTGG TGGAGGCCTG GTACAGCCTG GGGGTTCTCT GAGACTCTCC	120
TGTGCAACTT CTGGGTTTAC CTTCAGTGAT TTCTACATGG AGTGGGTCCG CCAGCCTCCA	180
GGGAAGAGAC TGGAGTGGAT TGCTGCAAGT AGAAAGAAAG CTAATGATTA TAAAACAGAG	240
TACAGTGCAT CTGTGAAGGG GCGGTTTACC GTCTCCAGAG ACACTTCCCA AAGCATCCTC	300
TACCTTCAGA TGAATGCCCT GAGAGATGAG GACACTGCCA TTTATTACTG TGCAAGAGAT	360
GCACGGCAGC TCGGGCTCCC GTTTGCTTAC TGGGGCCAAG GGACTCTGGT CACTGTCTCT	420
GCA	423

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGGAATCAC AGACTCTGGT CTTTCATATCC ATACTGCTCT GGTATATATGG AGCTGATGGG 60
AACATTGTAA TGACCCAATC TCCCAAATCC ATGTCCATGT CAGTAGGAGA GAGGGTCACC 120
TTGACCTGCA AGGCCAGTGA GAATGTGGTT ACTTATGTTT CCTGGTATCA ACAGAAACCA 180
GAGCAGTCTC CTAAACTGCT GATATACGGG GCATCCAACC GGTACACTGG GTCCCCGAT 240
CGCTTCACAG GCAGTGGATC TGCAACAGAT TTCACTCTGA CCATCAGCAG TGTGCAGGCT 300
GAAGACCTTG CAGATTATCA CTGTGGACAG GGTTACAGCT ATCCGTACAC GTTCCGAGGG 360
GGGACCAAGC TGGAAATAAA ACGG 384

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 402 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGACATGA GGGCTCCTGC ACAGATTTTT GGCTTCTTGT TGCTCTTGTT TCAAGGTACC 60
AGATGTGACA TCCAGATGAC CCAGTCTCCA TCCTCCTTAT CTGCCTCTCT GGGAGAAAGA 120
GTCAGTCTCA CTTGTCGGGC AAGTCAGGAC ATTGGTAGTA GCTTAACTG GCTTCAGCAG 180
GAACCAGATG GAACTATTAA ACGCCTGATC TACGCCACAT CCAGTTTAGA TTCTGGTGTG 240
CCCAAAAGGT TCAGTGGCAG TAGGTCTGGG TCAGATTATT CTCTCACCAT CAGCAGCCTT 300
GAGTCTGAAG ATTTTGTAGA CTATTACTGT CTACAATATG CTAGTTCTCC GTACACGTTT 360

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GGAGGGGGGA CCAAGCTGGA AATAAAACGG GCTGATGCTT CA

402

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGGAGTCAC AGATTCAGGT CTTTGTATTC GTGTTTCTCT GGTTGTCTGG TGTTGACGGA	60
GACATTGTGA TGACCCAGTC TCACAAATTC ATGTCCACTT CAGTAGGAGA CAGGGTCAGC	120
ATCACCTGCA AGGCCAGTCA GGATGTGAGT ACTGCTGTAG CCTGGTATCA ACAGAAACCA	180
GGACAATCTC CTAAACTACT GATTTACTCG GCATCCTACC GGTACACTGG AGTCCCTGAT	240
CGCTTCACTG GCAGTGGATC TGGGACGGAT TTCACTTTCA CCATCAGCAG TGTGCAGGCT	300
GAAGACCTGG CAGTTTATTA CTGTCAGCAA CATTATACTA CTCCGCTCAC GTTCGGTGCT	360
GGGACCAGGC TGGAGCTGAA ACGGGCTGAT GCTTCA	396

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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ATGGCTGTCT TGGGGCTGCT CTTCTGCCTG GTGACATTCC CAAGCTGTGT CCTATCCCAG	60
GTGCAGCTGA GGCAGTCAGG ACCTGGCCTA GTGCAGCCCT CACAGAGCCT GTCCATCACC	120
TGCACAGTCT CTGGTTTCTC ATTAAC TAGC TATGGTGTAC ACTGGTTTCG CCAGTCTCCA	180
GGAAAGGGTC TGGAGTGGCT GGGAGTGATA TGGAGTGGTG GAAGCACAGA CTATAATGCA	240
GCTTTCATAT CCAGACTGAG CATCAGCAAG GACAATTCCA AGAGCCAAGT TTTCTTTAAA	300
ATGAACAGTC TGCAAGCTAA TGACACAGCC ATATATTACT GTGCCAGAAA TAGGGGTAGG	360
TACAATTACT ATGCTATGGA CTACTGGGGT CAAGGAACCT CAGTCACCGT CTCCTCA	417

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGGAATCAC AGACTCTGGT CTTTCATATCC ATACTGCTCT GGTTATATGG AGCTGATGGG	60
AACATTGTAA TGACCCAATC TCCCAAATCC ATGTCCATGT CAGTAGGAGA GAGGGTCACC	120
TTGACCTGCA AGGCCAGTGA GAATGTGGTT ACTTATGTTT CNTGGTATCA ACAGAAACCA	180
GAGCAGTCTC CTAAACTGCT GATATATGGG GCATCCAACC GGTACACTGG GGTCCCNGAT	240
CGCTTCACAG GCAGTGGATC TGCAACAGAT TTTACTCTGA CCATCAGCAG TGTGCAGGCT	300
GAAGACCTTG CAGATTATCA CTGTGGACAG GGTACAGCT ATCCGTACAC GTTCCGAGGG	360
GGGACCAAGC TGAAAATAAA ACGG	384

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGGGATGGA GATGGATCTT TCTTTTCCTC CTGTCAGGAA CTGCAGGTGT CCATTGCCAG 60
GTTTCAGCTGC AGCAGTCTGG ACCTGAGCTG GTGAAGCCTG GGGCTTTAGT GAAGATATCC 120
TGCAAGGCTT CTGGTTACAC CTTTACAAGC TACGATATAA ACTGGGTGAA GCAGAGGCCCT 180
GGACAGGGAC TTGAGTGGAT TGGATGGATT TATCCTGGAG ATGGTAGTAC TAAGTACAAT 240
GAGAAATTCA AGGGCAAGGC CACACTGACT GCAGACAAAT CCTCCAGCAC AGCCTACATG 300
CAGCTCAGCA GCCTGACTTC TGAGAACTCT GCAGTCTATT TCTGTGCAAG A 351

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TACTGGTACT TCGATGTCTG GGGCGCAGGG ACCACGGTCA CCGTTTCCTC AGAGAGT 57

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGGCTGTCT TGGGGCTGCT CTTCTGCCTG GTGACATTCC CAAGCGGTGT CCTATCCCAG	60
GTGCAGCTGA AGCAGTCAGG ACCTGGCCTA GTGCAGCCCT CACAGAGCCT GTCCATCACC	120
TGCACAGTCT CTGGTTTCTC ATTAAC TAGC TATGGTGTAC ACTGGGTTCG CCAGTCTCCA	180
GGAAAGGGTC TGGAGTGGCT GGGAGTGATA TGGAGTGGTG GAAGCACAGA CTATAATGCA	240
GCTTTCATAT CCAGACTGAG CATCAGCAAG GACAATTCCA AGAGCCAAGT TTTCTTTAAA	300
ATGAACAGTC TGCAAGCTAA TGACACAGCC ATATATTACT GTGCCAGA	348

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGGCTGTCT TAGGGCTGCT CTTCTGCCTA GTGACATTCC CAAGCGGTGT CCTATCCCAG	60
GTGCAGCTGA AGCAGTCAGG ACCTGGCCTA GTGCAGCCCT CACAGAGCCT GTCCATCACC	120
TGCACAGTCT CTGGTTTCTC ATTAAC TAGC TATGGTGTAC ACTGGGTTCG CCAGTCTCCA	180
GGAAAGGGTC TGGAGTGGCT GGGAGTGATA TGGAGTGGTG GAAGCACAGA CTATAATGCA	240
GCTTTCATAT CCAGACTGAG CATCAGCAAG GACAATTCCA AGAGCCAAGT TTTCTTTAAA	300
ATGAACAGTC TGCAATCTAA TGACACAGCC ATATATTACT GTGCCAGA	348

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

468720-48026980

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TACTATGCTA TGGACTACTG GGGTCAAGGA ACCTCAGTCA CCGTCTCCTC A

51

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGAAGTTGT GGTAAACTG GGTTCCTT TTAACACTTT TACATGGTAT CCAGTGTGAG	60
GTGAAGCTGG TGGAATCTGG AGGAGGCTTG GTACAGCCTG GGGGTTCTCT GAGACTCTCC	120
TGTGCAACTT CTGGGTTTAC CTTCAGTGAT TTCTACATGG AGTGGGTCCG CCAGCCTCCA	180
GGGAAGAGAC TGGAGTGGAT TGCTGCAAGT AGAAACAAAG CTAATGATTA TACAACAGAG	240
TACAGTGCAT CTGTGAAGGG TCGGTTTCATC GTCTCCAGAG ACACTTCCCA AAGCATCCTC	300
TACCTTCAGA TGAATGCCCT GAGAGCTGAG GACACTGCCA TTTATTACTG TGCAAGAGAT	360
GCAC	364

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

0069204-01897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCCTGGTTTG CTTACTGGGG CCAAGGGACT CTGGTCACTG TCTCTGCA

48

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGGACATGA GGGCTCCTGC ACAGATTTTT GGCTTCTTGT TGCTCTTGTT TCAAGGTACC	60
AGATGTGACA TCCAGATGAC CCAGTCTCCA TCCTCCTTAT CTGCCTCTCT GGGAGAAAGA	120
GTCAGTCTCA CTTGTCGGGC AAGTCAGGAC ATTGGTAGTA GCTTAAACTG GCTTCAGCAG	180
GAACCAGATG GAACTATTAA ACGCCTGATC TACGCCACAT CCAGTTTAGA TTCTGGTGTG	240
CCCAAAGGT TCAGTGGCAG TAGGTCTGGG TCAGATTATT CTCTCACCAT CAGCAGCCTT	300
GAGTCTGAAG ATTTTGTAGA CTATTACTGT CTACAATATG CTAGTTCCTCC G	351

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGGACATGA GGGCTCCTGC ACAGATTTTT GGCTTCTTGT TGCTCTTGTT TCAAGGTACC	60
AGATGTGACA TCCAGATGAC CCAGTCTCCA TCCTCCTTAT CTGCCTCTCT GGGAGAAAGA	120

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GTCAGTCTCA CTTGTCGGGC AAGTCAGGAC ATTGGTAGTA GCTTAAACTG GCTTCAGCAG 180
 GAACCAGATG GAACTATTAA ACGCCTGATC TACGCCACAT CCAGTTTAGA TTCTGGTGTC 240
 CCCAAAAGGT TCAAGTGGCAG TAGGTCTGGG TCAGATTATT CTCTCACCAT CAGCAGCCTT 300
 GAGTCTGAAG ATTTTGTAGA CTATTACTGT CTACAATATG CTAGTTCTCC T 351

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TACACGTTTCG GAGGGGGGAC CAAGCTGGAA ATAAAACGGG CTGATGCTTC A 51

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTCACGTTTCG GTGCTGGGAC CAAGCTGGAG CTGAAACGGG CTGATGCTTC A 51

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 393 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATG ATG TCC TCT GCT CAG TTC CTT GGT CTC CTG TTG CTC TGT TTT CAA	48
Met Met Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Cys Phe Gln	
1 5 10 15	
GGT ACC AGA TGT GAT ATC CAG ATG ACA CAG ACT ACA TCC TCC CTG TCT	96
Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser	
20 25 30	
GCC TCT CTG GGA GAC AGA GTC ACC ATC AGT TGC AGG GCA AGT CAG GAC	144
Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp	
35 40 45	
ATT AGC AAT TAT TTA AAC TGG TAT CAG CAG AAA CCA GAT GGA ACT GTT	192
Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val	
50 55 60	
AAA CTC CTG ATC TAC TAC ACA TCA AGA TTA CAC TCA GGA GTC CCA TCA	240
Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser	
65 70 75 80	
AGG TTC AGT GGC AGT GGG TCT GGA ACA GAT TAT TCT CTC ACC ATT AGC	288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser	
85 90 95	
AAC CTG GAG CAA GAA GAT ATT GCC ACT TAC TTT TGC CAA CAG GGT AAT	336
Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn	
100 105 110	
ACG CTT CCG TGG ACG TTC GGT GGA GGC ACC AAG CTG GAA ATC AAA CGG	384
Thr Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg	
115 120 125	
GCT GAT GCT	393

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Ala Asp Ala
130

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Met Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Leu Cys Phe Gln
1 5 10 15

Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser
20 25 30

Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp
35 40 45

Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val
50 55 60

Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser
85 90 95

Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn
100 105 110

Thr Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
115 120 125

Ala Asp Ala
130

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(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATATCCAGA TGACACAGAC TACATCCTCC CTGTCTGCCT CTCTGGGAGA CAGAGTCACC	60
ATCAGTTGCA GGGCAAGTCA GGACATTAGC AATTATTTAA ACTGGTATCA GCAGAAACCA	120
GATGGAAGT TTAAGTCTCT GATCTACTAC ACATCAAGAT TACACTCAGG AGTCCCATCA	180
AGGTTTCAGT GCAGTGGGTC TGGAACAGAT TATTCTCTCA CCATTAGCAA CCTGGAGCAA	240
GAAGATATTG CCACTTACTT TTGCCAACAG GGTAATACGC TTCCTCCGAC GTTCGGTGGG	300
GGCACCAAGC TGGAAATCAA ACGG	324

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATATCCAGA TGACACAGAC TACATCCTCC CTGTCTGCCT CTCTGGGAGA CAGAGTCACC	60
ATCAGTTGCA GGGCAAGTCA GGACATTAGC AATTATTTAA ACTGGTATCA GCAGAAACCA	120
GATGGAAGT TTAAGTCTCT GATCTACTAC ACATCAAGAT TACACTCAGG AGTCCCATCA	180

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AGGTTTCAGTG GCAGTGGGTC TGGAACAGAT TATTCTCTCA CCATTAGCAA CCTGGAGCAA 240

GAAGATATTG CCACTTACTT TTGCCAACAG GGTAATACGC TTCCT 285

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGGACGTTTCG GTGGAGGCAC CAAGCTGGAA ATCAAACGT 39

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 429 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTT	TTG	GTA	GCA	GCA	GCT	ACA	GGT	48
Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Ala	Ala	Thr	Gly	
1				5					10					15		

GTC	CAC	TCC	CAG	GTC	CAA	CTG	CAG	CAG	CCT	GGG	ACT	GAA	CTG	GTG	AAG	96
Val	His	Ser	Gln	Val	Gln	Leu	Gln	Gln	Pro	Gly	Thr	Glu	Leu	Val	Lys	
			20					25					30			

CCT	GGG	GCT	TCA	GTG	AAG	CTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	144
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Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

ACC AGC TAC TGG ATG CAC TGG GTG AAG CAG AGG CCT GGA CAA GGC CTT 192
Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
50 55 60

GAG TGG ATT GGA AAT ATT AAT CCT AGC AAT GGT GGT ACT AAC TAC AAT 240
Glu Trp Ile Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn
65 70 75 80

GAG AAG TTC AAG AGC AAG GCC ACA CTG ACT GTA GAC AAA TCC TCC AGC 288
Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
85 90 95

ACA GCC TAC ATG CAG CTC AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC 336
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

TAT TAT TAT GCA AGA CGG GCC CCT TAC TAC GGT AGT AGG AAC TTT GAC 384
Tyr Tyr Tyr Ala Arg Arg Ala Pro Tyr Tyr Gly Ser Arg Asn Phe Asp
115 120 125

TAC TGG GGC CAA GGC ACC ACT CTC ACA GTC TCC TCA GAG AGT CAG 429
Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Glu Ser Gln
130 135 140

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

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Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys
20 25 30

Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
50 55 60

Glu Trp Ile Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn
65 70 75 80

Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Tyr Ala Arg Arg Ala Pro Tyr Tyr Gly Ser Arg Asn Phe Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Glu Ser Gln
130 135 140

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CAG GTC CAA CTG CAG CAG CCT GGG ACT GAA CTG GTG AAG CCT GGG GCT
Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

TCA GTG AAG CTG TCC TGC AAG GCT TCT GGC TAC ACC TTC ACC AGC TAC 96
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

TGG ATG CAC TGG GTG AAG CAG AGG CCT GGA CAA GGC CTT GAG TGG ATT 144
Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

GGA AAT ATT AAT CCT AGC AAT GGT GGT ACT AAC TAC AAT GAG AAG TTC 192
Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

AAG AGC AAG GCC ACA CTG ACT GTA GAC AAA TCC TCC AGC ACA GCC TAC 240
Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

ATG CAG CTC AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC TAT TAT TAT 288
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Tyr
85 90 95

GCA AGA GAT TAC TAC GGT AGT AGC TGG GGG TAC TAC TTT GAC TAC TGG 336
Ala Arg Asp Tyr Tyr Gly Ser Ser Trp Gly Tyr Tyr Phe Asp Tyr Trp
100 105 110

GGC CAA GGC ACC ACT CTC ACA GTC TCC TCA 366
Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
115 120

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

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Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Tyr
85 90 95

Ala Arg Asp Tyr Tyr Gly Ser Ser Trp Gly Tyr Tyr Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
115 120

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATGGGATGGA GCTGTATCAT CCTCTTTTGG GTAGCAGCAG CTACAGGTGT CCACTCCCAG	60
GTCCAAGTGC AGCAGCCTGG GACTGAACTG GTGAAGCCTG GGGCTTCAGT GAAGCTGTCC	120
TGCAAGGCTT CTGGCTACAC CTTCACCAGC TACTGGATGC ACTGGGTGAA GCAGAGGCCT	180
GGACAAGGCC TTGAGTGGAT TGGAAATATT AATCCTAGCA ATGGTGGTAC TAACTACAAT	240

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GAGAAGTTCA AGAGCAAGGC CACACTGACT GTAGACAAAT CCTCCAGCAC AGCCTACATG 300

CAGCTCAGCA GCCTGACATC TGAGGACTCT GCGGTCATT ATTATGCAAG A 351

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TACTTTGACT ACTGGGGCCA AGGCACCACT CTCACAGTCT CCTCA 45

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met	Gly	Trp	Arg	Trp	Ile	Phe	Leu	Phe	Leu	Leu	Ser	Gly	Thr	Ala	Gly
1				5					10					15	

Val	His	Cys	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Lys
			20				25						30		

Pro	Gly	Ala	Leu	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
		35					40					45			

Thr	Ser	Tyr	Asp	Ile	Asn	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu
	50						55				60				

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Glu Trp Ile Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn
65 70 75 80

Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asn Ser Ala Val
100 105 110

Tyr Phe Cys Ala Arg Gly Ala Arg Phe Tyr Trp Tyr Phe Asp Val Trp
115 120 125

Gly Ala Gly Thr Thr Val Thr Val Ser Ser
130 135

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Ala Val Leu Gly Leu Leu Phe Cys Leu Val Thr Phe Pro Ser Cys
1 5 10 15

Val Leu Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln
20 25 30

Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu
35 40 45

Thr Ser Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu
50 55 60

Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ala
65 70 75 80

Ala Phe Ile Ser Arg Leu Ser Ile Ser Lys Asp Ala Ser Lys Ser Gln
85 90 95

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Val Phe Phe Lys Met Asn Ser Leu His Ala Thr Asp Thr Ala Ile Tyr
 100 105 110

Tyr Cys Ala Arg Asp Tyr Gly Ser Arg Gly Asp Tyr Trp Gly Gln Gly
 115 120 125

Thr Ser Val Thr Val Ser Ser
 130 135

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Lys Leu Trp Leu Asn Trp Val Phe Leu Leu Thr Leu Leu His Gly
 1 5 10 15

Ile Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe
 35 40 45

Ser Asp Phe Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu
 50 55 60

Glu Trp Ile Ala Ala Ser Arg Lys Lys Ala Asn Asp Tyr Lys Thr Glu
 65 70 75 80

Tyr Ser Ala Ser Val Lys Gly Arg Phe Thr Val Ser Arg Asp Thr Ser
 85 90 95

Gln Ser Ile Leu Tyr Leu Gln Met Asn Ala Leu Arg Asp Glu Asp Thr
 100 105 110

Ala Ile Tyr Tyr Cys Ala Arg Asp Ala Arg Gln Leu Gly Leu Pro Phe
 115 120 125

268120-18026980

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
130 135 140

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met	Glu	Ser	Gln	Thr	Leu	Val	Phe	Ile	Ser	Ile	Leu	Leu	Trp	Leu	Tyr	
1				5					10					15		
Gly	Ala	Asp	Gly	Asn	Ile	Val	Met	Thr	Gln	Ser	Pro	Lys	Ser	Met	Ser	
			20					25					30			
Met	Ser	Val	Gly	Glu	Arg	Val	Thr	Leu	Thr	Cys	Lys	Ala	Ser	Glu	Asn	
		35					40					45				
Val	Val	Thr	Tyr	Val	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Glu	Gln	Ser	Pro	
		50					55				60					
Lys	Leu	Leu	Ile	Tyr	Gly	Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	
65					70				75					80		
Arg	Phe	Thr	Gly	Ser	Gly	Ser	Ala	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	
				85					90					95		
Ser	Val	Gln	Ala	Glu	Asp	Leu	Ala	Asp	Tyr	His	Cys	Gly	Gln	Gly	Tyr	
			100					105					110			
Ser	Tyr	Pro	Tyr	Thr	Phe	Arg	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	
			115					120				125				

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids

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(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mus musculus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Asp Met Arg Ala Pro Ala Gln Ile Phe Gly Phe Leu Leu Leu Leu
1 5 10 15

Phe Gln Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

Leu Ser Ala Ser Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser
35 40 45

Gln Asp Ile Gly Ser Ser Leu Asn Trp Leu Gln Gln Glu Pro Asp Gly
50 55 60

Thr Ile Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val
65 70 75 80

Pro Lys Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr
85 90 95

Ile Ser Ser Leu Glu Ser Glu Asp Phe Val Asp Tyr Tyr Cys Leu Gln
100 105 110

Tyr Ala Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
115 120 125

Lys Arg
130

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

0303034-031692

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Glu Ser Gln Ile Gln Val Phe Val Phe Val Phe Leu Trp Leu Ser
1 5 10 15

Gly Val Asp Gly Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser
20 25 30

Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp
35 40 45

Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro
50 55 60

Lys Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Asp
65 70 75 80

Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser
85 90 95

Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr
100 105 110

Thr Thr Pro Leu Thr Phe Gly Ala Gly Thr Arg Leu Glu Leu Lys Arg
115 120 125

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met	Ala	Val	Leu	Gly	Leu	Leu	Phe	Cys	Leu	Val	Thr	Phe	Pro	Ser	Cys	1	5	10	15
Val	Leu	Ser	Gln	Val	Gln	Leu	Arg	Gln	Ser	Gly	Pro	Gly	Leu	Val	Gln	20	25	30	
Pro	Ser	Gln	Ser	Leu	Ser	Ile	Thr	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	35	40	45	
Thr	Ser	Tyr	Gly	Val	His	Trp	Phe	Arg	Gln	Ser	Pro	Gly	Lys	Gly	Leu	50	55	60	
Glu	Trp	Leu	Gly	Val	Ile	Trp	Ser	Gly	Gly	Ser	Thr	Asp	Tyr	Asn	Ala	65	70	75	80
Ala	Phe	Ile	Ser	Arg	Leu	Ser	Ile	Ser	Lys	Asp	Asn	Ser	Lys	Ser	Gln	85	90	95	
Val	Phe	Phe	Lys	Met	Asn	Ser	Leu	Gln	Ala	Asn	Asp	Thr	Ala	Ile	Tyr	100	105	110	
Tyr	Cys	Ala	Arg	Asn	Arg	Gly	Arg	Tyr	Asn	Tyr	Tyr	Ala	Met	Asp	Tyr	115	120	125	
Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	130	135							

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